

Assessment of *Aegilops tauschii* for Resistance to Biotypes of Wheat Curl Mite (Acari: Eriophyidae)

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ABSTRACT *Aegilops tauschii*, the wild diploid D-genome progenitor of wheat, *Triticum aestivum* L., is an important source of resistance to several arthropod pests and pathogens. A total of 108 *Ae. tauschii* accessions from different geographic regions were evaluated for resistance to biotypes of the wheat curl mite, *Aceria tosicella* Keifer, from Kansas, Nebraska, and Montana. The wheat curl mite is the only vector known to transmit wheat streak mosaic virus. Wheat curl mite resistance was detected in germplasm from all the geographic locations represented. The highest percentage of resistant accessions originated from Turkey, followed by Afghanistan and the Caspian Sea region of Iran. Sixty-seven percent of the accessions exhibited resistance to at least one wheat curl mite biotype and 19% were resistant to all the three biotypes. Resistance to the accessions tested occurred more frequently in the Nebraska and Kansas biotypes (69% and 64%, respectively) than did resistance to the Montana biotype (42%), although the frequency of resistance was not significant. The differential reactions of accessions to the different wheat curl mite biotypes suggests that *Ae. tauschii* has at least five different genes for resistance to mite colonization. *Ae. tauschii* continues to be a very useful source for wheat curl mite resistance genes for bread wheat improvement.

KEY WORDS *Aceria tosicella*, *Aegilops tauschii*, *Triticum aestivum*, plant resistance

GENETIC RESISTANCE IN CROP plants is the most economical and environmentally safe method for decreasing yield losses as a result of pest attacks (Smith 1999). However, although plant resistance to arthropods is very effective, resistance in crop cultivars is not always permanent. Deploying resistance genes often imposes selection pressure on pest populations and can lead to development of virulent pest biotypes (strains or races) (Smith 1989). The Hessian fly, *Mayetiola destructor* (Say), and the greenbug, *Schizaphis graminum* (Rondani) have developed virulence to deployed resistance genes in wheat (Ratcliffe et al. 2000, Porter et al. 1997). A continuous search for new sources of resistance is required to combat the development of biotypes and the loss of effectiveness of arthropod-resistant wheat cultivars.

Six different biotypes of the wheat curl mite, *Aceria tosicella* Keifer, from Kansas, Nebraska, Montana, Alberta, Canada, South Dakota, and Texas, vary in virulence and can be identified by their response to resistance genes in different grasses (Harvey et al. 1995, 1999). Different mite collections also vary in

their ability to transmit wheat streak mosaic virus (WSMV) and high plains virus (HPV) (Seifers et al. 2002).

Aegilops tauschii (Coss) Schmal. is used widely as a source of useful genes for improvement of common wheat (*Triticum aestivum* L., 2n = 6X = 42, AABBDD). Several arthropod-resistance genes have been transferred from *Ae. tauschii* to common wheat, including genes for resistance to the wheat curl mite (Thomas and Conner 1986), the Hessian fly (Hatchett et al. 1981, Cox and Hatchett 1994, Raupp et al. 1993) and the greenbug (Gill et al. 1991). The D-genome of this species is completely homologous to and recombines freely with the D-genome of common wheat (Riley and Chapman 1960, Thomas and Whelan 1991). Direct transfers of genes from *Ae. tauschii* to hexaploid wheat have been accomplished, including the *Cmc1* and *Cmc4* genes conferring resistance to wheat curl mite (Thomas and Conner 1986, Cox et al. 1999, Malik et al. 2003).

Aegilops tauschii is comprised of the subspecies *strangulata* and *tauschii*. Subspecies *strangulata* is commonly found in Transcaucasia and southeastern Iran near the Caspian Sea, and subspecies *tauschii* is found in northcentral Iran and southwestern Caspian Iran. Molecular studies by Dvorak et al. (1998) indicate that *T. aestivum* is most closely related to *Ae. tauschii* ssp. *strangulata* from Transcaucasia, particularly from Armenia and southwestern Caspian Iran.

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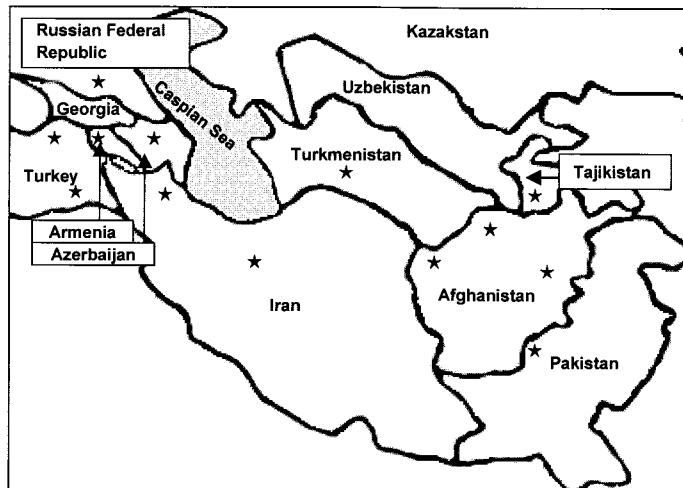


Fig. 1. Geographic distribution of *Ae. tauschii* accessions evaluated for resistance to the wheat curl mite. Stars show the location of accession collections. Accessions collected from Japan and Portugal are not shown.

The objective of this study was to evaluate a group of 108 *Ae. tauschii* accessions for resistance to three different biotypes of the wheat curl mite from the central Great Plains of North America.

Materials and Methods

Seeds of 108 *Ae. tauschii* accessions were obtained from the Wheat Genetic Resource Center (WGRC) collection at Kansas State University, Manhattan, KS. Twelve accessions were of the subspecies *strangulata* and 95 accessions were of the subspecies *tauschii*. The accessions evaluated were from Afghanistan, Turkey, Iran, Georgia, Russia, Azerbaijan, Tajikistan, Turkmenistan, and Pakistan (Fig. 1). Their geographic distribution ranged from latitude N30.00 (Balochistan, Pakistan) to N 42.03 (Dagestan, Russian Federal Republic) and longitude E43.05 (Kars, Turkey) to E69.44 (Tajikistan). The origin of twelve accessions is unknown. Sixty-nine percent of the accessions evaluated were from Afghanistan, Iran, and Turkey (Table 1).

In the first experiment, 47 accessions previously identified as resistant to the Alberta, Canada, wheat curl mite biotype were evaluated. In the second experiment, 15 accessions susceptible to the Alberta biotype plus 46 accessions selected at random were evaluated. In both experiments, accessions were evaluated for resistance to wheat curl mite biotypes from Kansas, Montana, and Nebraska. Sixty-one percent of the accessions were evaluated for their reaction to all three biotypes, and 86%, 72%, and 61% of the accessions were screened for resistance to the Kansas, Montana, and Nebraska biotypes, respectively.

Phenotypic screening was conducted by infesting *Ae. tauschii* seedlings at the two leaf stage of development grown in dyna-flats (10 × 10 × 50 cm, Hummert International). One hundred and fifty plants were grown in each flat. The different accessions were randomly planted with 8–10 seedlings of the same

accession in a row. Ten nonviruliferous mites, counted under a 7× microscope with a fiber optic illumination system, were placed in the whorl of the second leaf of each plant with a very fine moist artist brush. The inoculated plants were grown at 20–25°C with a photoperiod of 16:8 (L:D) h. Wheat curl mite-susceptible controls included were 'Tomahawk', 'Jagger', and 'Wichita'. The resistant controls were KS96WGRC40 (*Cmc4*) and 'TAM107' (*Cmc3*). Plants were scored individually for resistance or susceptibility between 7 and 14 d postinfestation, depending on the degree of symptom expression in the susceptible control plants. Plants with normal leaves were classified as resistant and plants with curled or trapped leaves were classified as susceptible. Wheat curl mite damage data were grouped by *Ae. tauschii* accession origin and subspecies. Data were subjected to chi-square analyses (Steel and Torrie 1960) to determine differences in the frequency of resistance in the accessions evaluated to the Kansas, Montana, and Nebraska biotypes.

The experiments were conducted in several subsets, consisting of *Ae. tauschii* accessions that were tested simultaneously, in different greenhouses, with the three different wheat curl mite biotypes. To prevent cross-contamination, biotypes were reared separately in cages on plants of 'Tomahawk' wheat in separate greenhouses. The Kansas biotype originated in Ellis county Kansas in 1996. The Montana and Nebraska biotypes were provided by Dr. Sue Blodgett and Dr. Talat Mohamood, respectively, in 1996.

Results

Of the 108 *Ae. tauschii* accessions evaluated, 72 were resistant to at least one of the three wheat curl mite biotypes (Table 1). Of the 66 accessions tested with all three biotypes, 21 accessions were resistant to all biotypes and 12 accessions were susceptible to all biotypes. All of the susceptible control plant leaves were

Table 1. Seventy-two *Ae. tauschii* accessions expressing resistance to at least one wheat curl mite biotype

WCRC Accession no.	Taxonomic group	Origin	Wheat curl mite biotype		
			Montana	Kansas	Nebraska
TA1577	<i>tauschii</i>	Unknown	R	R	R
TA1578	<i>tauschii</i>	Unknown	R	R	R
TA1580	<i>tauschii</i>	Unknown	R	R	R
TA1582	<i>tauschii</i>	Turkey	S	R	— ^a
TA1583	<i>tauschii</i>	Turkey	S	R	—
TA1584	<i>tauschii</i>	Turkey	S	R	—
TA1585	<i>tauschii</i>	Turkey	S	R	—
TA1587	<i>tauschii</i>	Turkey	S	R	—
TA1588	<i>tauschii</i>	Turkey	R	R	R
TA1589	<i>tauschii</i>	Turkey	R	S	R
TA1590	<i>tauschii</i>	Turkey	S	R	—
TA1591	<i>tauschii</i>	Turkey	S	R	R
TA1592	<i>tauschii</i>	Turkey	S	R	R
TA1593	<i>tauschii</i>	Turkey	R	R	R
TA1594	<i>tauschii</i>	Turkey	S	R	R
TA1596	<i>tauschii</i>	Turkey	R	S	S
TA1597	<i>tauschii</i>	Turkey	S	R	—
TA1604	<i>typica</i>	Afghanistan	S	R	—
TA1606	<i>tauschii</i>	Iran	S	R	—
TA1612	<i>tauschii</i>	Former USSR	S	R	—
TA1613	<i>strangulata</i>	Russian Federal	S	R	—
TA1616	<i>tauschii</i>	Russian Federal	—	R	—
TA1617	<i>tauschii</i>	Turkmenistan	S	R	—
TA1618	<i>strangulata</i>	Iran	R	R	R
TA1619	<i>meyeri</i>	Iran	S	R	—
TA1621	<i>tauschii</i>	Georgia	R	R	R
TA1624	<i>strangulata</i>	Azerbaijan	S	R	—
TA1625	<i>tauschii</i>	Azerbaijan	R	R	R
TA1626	<i>strangulata</i>	Turkmenistan	S	R	—
TA1630	<i>tauschii</i>	Afghanistan	S	R	—
TA1639	<i>tauschii</i>	Afghanistan	R	R	R
TA1645	<i>strangulata</i>	Iran	R	S	S
TA1652	<i>tauschii</i>	Tajikistan	—	S	R
TA1655	<i>tauschii</i>	Afghanistan	S	R	R
TA1676	<i>tauschii</i>	Azerbaijan	R	R	R
TA1695	<i>strangulata</i>	Japan	—	R	R
TA1697	<i>anathera</i>	Japan	—	R	R
TA1712	<i>tauschii</i>	Portugal	—	R	R
TA2379	<i>typica</i>	Pakistan	R	R	R
TA2381	<i>anathera</i>	Pakistan	R	R	—
TA2382	<i>anathera</i>	Pakistan	R	S	R
TA2383	<i>typica</i>	Pakistan	R	R	R
TA2386	<i>typica</i>	Pakistan	R	R	R
TA2389	<i>typica</i>	Afghanistan	—	R	R
TA2390	<i>typica</i>	Afghanistan	—	R	R
TA2394	<i>typica</i>	Afghanistan	—	R	S
TA2395	<i>typica</i>	Afghanistan	—	R	R
TA2397	<i>typica</i>	Afghanistan	R	R	R
TA2402	<i>typica</i>	Afghanistan	—	S	R
TA2403	<i>typica</i>	Afghanistan	—	R	R
TA2406	<i>typica</i>	Afghanistan	R	R	R
TA2407	<i>anathera</i>	Afghanistan	R	R	R
TA2411	<i>typica</i>	Afghanistan	—	R	R
TA2414	<i>typica</i>	Afghanistan	—	S	R
TA2417	<i>anathera</i>	Afghanistan	R	—	—
TA2419	<i>typica</i>	Afghanistan	R	S	R
TA2457	<i>typica</i>	Iran	R	R	R
TA2483	<i>typica</i>	Iran	R	R	R
TA2493	<i>typica</i>	Iran	R	S	R
TA2509	<i>typica</i>	Turkey	R	R	R
TA2510	<i>typica</i>	Turkey	—	R	—
TA2519	<i>typica</i>	Iran	R	R	R
TA2531	<i>typica</i>	Afghanistan	—	S	R
TA2532	<i>typica</i>	Afghanistan	—	R	R
TA2537	<i>typica</i>	Afghanistan	—	S	R
TA2538	<i>typica</i>	Afghanistan	—	R	R
TA2544	<i>typica</i>	Afghanistan	—	R	—
TA2556	<i>anathera</i>	Afghanistan	R	R	—
TA2557	<i>anathera</i>	Afghanistan	R	S	—
TA2579	<i>typica</i>	Afghanistan	—	R	—
TA2587	<i>typica</i>	Afghanistan	R	R	R
TA2695	Unknown	Unknown	—	R	R

^a Not evaluated.

Table 2. Numbers of *Ae. tauschii* subspecies *tauschii* and *strangulata* accessions from different geographic areas classified as resistant (R) or susceptible (S) to biotypes of wheat curl mite from Montana, Kansas, and Nebraska

<i>Ae. tauschii</i> origin	Wheat curl mite biotype								
	Montana			Kansas			Nebraska		
	R	S	χ^2	R	S	χ^2	R	S	χ^2
Turkey	4	12	0.5000	13	3	0.7813	7	2	0.3472
Afghanistan	9	14	0.1359	20	16	0.0556	19	9	0.4464
Iran	6	9	0.0750	6	4	0.0500	5	3	0.0625
Other ^a	12	11	0.0054	22	9	0.6815	17	6	0.6576
Total	31	46	0.3653	61	32	1.1304	48	20	1.4412
Subspecies									
<i>tauschii</i>	32	39	0.0863	57	30	1.0474	46	18	1.5313
<i>strangulata</i>	8	2	0.4500	5	4	0.0139	2	3	0.0250

All χ^2 values are not significant, $P = 0.05$.

^aAzerbaijan, former USSR, Federal Russia, Georgia, Pakistan, Tajikistan, Turkmenistan, and accessions of unknown origin.

either tightly curled or trapped when infested with each of the three biotypes, whereas plants of the resistant controls were normal and unaffected.

Resistance in *Ae. tauschii* was observed in 48 of 68 accessions evaluated with the Nebraska biotype (71%), in 61 of 93 accessions evaluated with the Kansas biotype (66%) and in 42% of the accessions evaluated to the Montana biotype (Table 2). Nevertheless, differences in the frequency of resistance within each of the three biotypes were nonsignificant ($P > 0.05$, $df = 1$). Overall, resistance to each biotype was observed in accessions from all the geographic regions tested in which *Ae. tauschii* is known to occur, but the frequency of resistance in accessions from each location was also nonsignificant ($P > 0.05$, $df = 1$) within each biotype (Table 2). Seven *Ae. tauschii* accessions of unknown origin were resistant to at least one biotype, and the one accession from Georgia was resistant to all three biotypes. Resistance was common in *Ae. tauschii* accessions collected west of the Caspian Sea (67%) and somewhat less frequent in accessions from the Caspian Sea area of Iran (53%).

Of the subspecies *tauschii* accessions, 70% were resistant to at least one biotype, whereas 50% of the subspecies *strangulata* accessions had resistance to at least one mite biotype (Table 1). Within subspecies *tauschii*, resistance was more frequent in the *typica* and *ananthera* varieties, compared with the *meyeri* variety (Table 1). Within the subspecies *tauschii*, 66% and 72% of the accessions were resistant to the Kansas and Nebraska biotypes, respectively, (Table 2) but neither frequency of resistance was significantly ($P > 0.05$, $df = 1$) greater than normal. Only 45% of the accessions evaluated were resistant to the Montana biotype. There were no significant differences in the frequency of resistance in the subspecies *strangulata* accessions to any of the three biotypes.

Discussion

Accessions originating from several geographic regions where *Ae. tauschii* is known to occur were assessed for wheat curl mite resistance in this study. However, because most accessions evaluated originated in Afghanistan, Turkey, and Iran, the level of

diversity of mite resistance in all geographic regions is likely yet to be fully determined.

There were no definite patterns of wheat curl mite resistance or susceptibility in *Ae. tauschii* across the range of latitude tested in this study. However, the highest frequency of resistance to at least one biotype was found in Turkey (82%), followed by Afghanistan (62%) and Iran (53%). Brown-Guedira et al. (1996) observed a high proportion of wheat curl mite resistance in *T. timopheevii* subsp. *araraticum* accessions from Turkey, Iraq, and Iran. Shevtchenko et al. (1970) documented the occurrence of wheat curl mites in Uzbekistan, Tashkent, and the Caucasian regions of central and northern Asia. The high occurrence of mite resistance in *Ae. tauschii* from Afghanistan, Turkey, and the Caucasian regions may be explained by the presence of wheat curl mite in these areas. Conversely, the low levels of mite resistance in accessions from Caspian Iran may be a result of a lack of wind dispersal of wheat curl mite over the Caspian Sea.

With one exception, all of the *Ae. tauschii* accessions evaluated for resistance to the Montana biotype had a response pattern similar to the Alberta, Canada, biotype (J. Thomas, unpublished data). Harvey et al. (1999) found similar reactions in the Montana and Alberta biotypes to different sources of resistance in common wheat. In addition, evaluation of the genetic variation of the rDNA ITS-1 gene between mite biotypes has also shown that the Montana and Alberta biotypes are similar (R. M. unpublished data). The results of the current study confirm these observations and add further evidence to support the hypothesis that the Montana and Alberta wheat curl mite biotypes are identical.

The differential reactions of accessions to the Kansas, Nebraska, and Montana biotypes of wheat curl mite suggest that *Ae. tauschii* has at least five different genes for resistance to mite colonization. Two named genes for mite resistance, *Cmc1* and *Cmc4*, have been transferred to wheat from *Ae. tauschii*. These genes differ in their reaction to the Nebraska biotype, which is virulent to *Cmc1* and avirulent to *Cmc4*. Five groups of *Ae. tauschii* accessions were identified based on their reaction to the biotypes tested in the current study. These include: (1) those resistant to each of the

biotypes tested; (2) those resistant to the Kansas and Nebraska biotypes but susceptible to the Montana biotype; (3) those resistant to only the Montana biotype; (4) those resistant to the Montana and Nebraska biotypes but susceptible to the Kansas biotype; and (5) those resistant to Kansas biotype, susceptible to the Nebraska biotype, and with an undetermined reaction to the Montana biotype.

From the results of the current study and others, we conclude that the resistance gene in *Ae. tauschii* accession TA2394 in group 5 may be the same as *Cmc1*, and that the group of accessions resistant to all the three biotypes may or may not contain *Cmc4*. In addition, accessions in groups 2, 3, and 4 appear to have resistance gene(s) that differ from *Cmc1* and *Cmc4*.

Several of the wheat curl mite-resistant *Ae. tauschii* accessions also are resistant to other wheat pests, including eyespot disease (*Pseudocercosporella herpotrichoides*), leaf rust (caused by *Puccinia triticina*), Hessian fly, and Septoria leaf blotch (caused by *Septoria tritici* Rob.) (Yildirim et al. 1995). The presence of multiple pest resistance genes in a single *Ae. tauschii* accession will be useful for transferring resistance to more than one pest at the same time. The wheat curl mite-resistant *Ae. tauschii* accessions identified in the current study should prove useful for transferring unique resistance genes to wheat cultivars in regions where different strains of wheat curl mite exist.

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